SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:
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(B) STREET: 4350 La Jolla Village Drive, 6th Floor
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24601-402I

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 base pairs

```
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

   (ii)  MOLECULE TYPE: Genomic DNA
   (iii) HYPOTHETICAL: NO
   (iv)  ANTISENSE: NO
   (v)   FRAGMENT TYPE:
   (vi)  ORIGINAL SOURCE:
   (ix)  FEATURE:

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:
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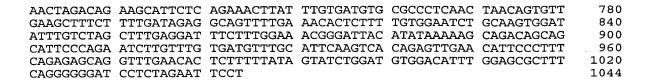
```
GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT    60
TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT   120
TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN   180
GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCCTC   240
GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNCC GTGATTTTCA GTTTTCTCGC   300
CAGATTCCAG GTCCTATAAT GTGCATTTCT CATTTNNCAC GTTTTTCAGT GATTTCGTCA   360
TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT   420
ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTC CACGCCATAT   480
TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTTCT CGCCATATTC   540
CAGGTCCTAC AGTGTGCATT CCTCATTTTT CACCTTTTTC ACTGATTTCG TCATTTTTCA   600
AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG   660
TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTTGACG   720
TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC   780
CTAATAGTGT GCATTCTCA TTTTTCACGT TTTTCAGTGA TTTCGTCATT TTTTCCAGTT   840
GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTTT CTTGCTATAT TCCATGTCCT   900
ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTC TCACCATATT TCACGTCCTA   960
AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA  1020
GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAATTTCTT CATTTTTTAA GCCCTCAAAT  1080
GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG  1140
ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTCATCGGC ACATTTCACG TCCTAAAGTG  1200
TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG  1260
CATTTCTCAT TTTTCACGTT TTTCAGTGAA TTC                                1293
```

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        (2)  INFORMATION FOR SEQ ID NO:2:

        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH: 1044 base pairs
             (B)  TYPE: nucleic acid
             (C)  STRANDEDNESS: single
             (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: Genomic DNA
        (iii) HYPOTHETICAL: NO
        (iv)  ANTISENSE: NO
        (v)   FRAGMENT TYPE:
        (vi)  ORIGINAL SOURCE:
        (ix)  FEATURE:

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:2:
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AGGCCTATGG TGAAAAGGA AATATCTTCC CCTGAAAACT AGACAGAAGG ATTCTCAGAA    60
TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTTT GATAGAGCAG   120
TTTTGAAACA CTCTTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC   180
CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT   240
TGGGATGTTT CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA   300
ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCGGTGAA   360
AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT   420
GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT   480
TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCGTTGG GAAACGGGAT   540
TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG   600
TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT   660
GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA   720
```

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AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT    780
GAAGCTTTCT TTTGATAGAG GCAGTTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT    840
ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG    900
CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT    960
CAGAGAGCAG GTTTGAACAC TCTTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT   1020
CAGGGGGGAT CCTCTAGAAT TCCT                                          1044
```

        (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2492 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:
        (ix) FEATURE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG     60
TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT    120
GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA    180
GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG    240
AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT    300
TGCTATCCTG GGGTTCAACC CCCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT    360
ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG    420
AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA    480
AGGGCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT    540
TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA    600
TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA    660
CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG    720
GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG    780
TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA    840
GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA    900
AGAGTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTTAAA AGAGTTTAGC AATTCTAACA    960
GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA   1020
ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG   1080
CATTTCTTGN NTTTNGGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT   1140
GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTC TTCAATATGA GGCTTGCTTT   1200
TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC   1260
TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAAATTC ATTACCAAAC CCAAAGGCAG   1320
ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG   1380
GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT   1440
CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTTGGG AAAGACACAG GATAGTGGGC   1500
TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA   1560
GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG   1620
CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA   1680
GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA   1740
GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA   1800
CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA   1860
ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC   1920
GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG   1980
GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT   2040
TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG   2100
GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA   2160
CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT   2220
TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT   2280
TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG   2340
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CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG      2400
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG      2460
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG                                    2492
```

        (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 28 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:
        (ix) FEATURE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GGGGAATTCA TTGGGATGTT TCAGTTGA                                          28
```

        (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 29 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:
        (ix) FEATURE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CGAAAGTCCC CCCTAGGAGA TCTTAAGGA                                         29
```

        (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 47 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: RNA
        (iii) HYPOTHETICAL: NO
        (iv) ANTISENSE: NO
        (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:
        (ix) FEATURE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC
```

        (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC   25

       (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 27 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: .
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA   27

       (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 69 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
    (D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT   48
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

GTC ACA AAC AGT GCA CCT ACT   69
Val Thr Asn Ser Ala Pro Thr

       (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 945 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

    (A) NAME/KEY: Coding Sequence
    (B) LOCATION: 1...942
    (D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

    PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG       48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
1               5                   10                  15

ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT       96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
                20                  25                  30

CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT      144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
            35                  40                  45

GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA      192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
        50                  55                  60

CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT      240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
65                  70                  75                  80

CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG      288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
                85                  90                  95

TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT      336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
                100                 105                 110

TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG      384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
            115                 120                 125

GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT      432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
        130                 135                 140

CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT      480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
145                 150                 155                 160

GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA      528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
                165                 170                 175

ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA      576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
                180                 185                 190

ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA      624
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Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
    195                 200                 205

TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT        672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
    210                 215                 220

GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT        720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
225                 230                 235                 240

AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG        768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
                245                 250                 255

TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC        816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
                260                 265                 270

GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT        864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
                275                 280                 285

TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG        912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
    290                 295                 300

TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA                            945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln
305                 310
```

        (2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:
    (ix) FEATURE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG   30

        (2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:
    (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTCAC   30

     (2) INFORMATION FOR SEQ ID NO:13:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1434 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: Genomic DNA
     (iii) HYPOTHETICAL: NO
     (iv) ANTISENSE: NO
     (v) FRAGMENT TYPE:
     (vi) ORIGINAL SOURCE:

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA      60
TGTCGACATT TCCACTCCCA ATGACGGTGA TGTATAATGC TCAAGTATTC TCCTGCTTTT     120
TTACCACTAA CTAGGAACTG GGTTTGGCCT TAATTCAGAC AGCCTTGGCT CTGTCTGGAC     180
AGGTCCAGAC GACTGACACC ATTAACACTT TGTCAGCCTC AGTGACTACA GTCATAGATG     240
AACAGGCCTC AGCTAATGTC AAGATACAGA GAGGTCTCAT GCTGGTTAAT CAACTCATAG     300
ATCTTGTCCA GATACAACTA GATGTATTAT GACAAATAAC TCAGCAGGGA TGTGAACAAA     360
AGTTTCCGGG ATTGTGTGTT ATTTCCATTC AGTATGTTAA ATTTACTAGG ACAGCTAATT     420
TGTCAAAAAG TCTTTTTCAG TATATGTTAC AGAATTGGAT GGCTGAATTT GAACAGATCC     480
TTCGGGAATT GAGACTTCAG GTCAACTCCA CGCGCTTGGA CCTGTCGCTG ACCAAAGGAT     540
TACCCAATTG GATCTCCTCA GCATTTTCTT TCTTTAAAAA ATGGGTGGGA TTAATATTAT     600
TTGGAGATAC ACTTTGCTGT GGATTAGTGT TGCTTCTTTG ATTGGTCTGT AAGCTTAAGG     660
CCCAAACTAG GAGAGACAAG GTGGTTATTG CCCAGGCGCT TGCAGGACTA GAACATGGAG     720
CTTCCCCTGA TATATGGTTA TCTATGCTTA GGCAATAGGT CGCTGGCCAC TCAGCTCTTA     780
TATCCCACGA GGCTAGTCTC ATTGTACGGG ATAGAGTGAG TGTGCTTCAG CAGCCCGAGA     840
GAGTTGCAAG GCTAAGCACT GCAATGGAAA GGCTCTGCGG CATATATGTG CCTATTCTAG     900
GGGGACATGT CATCTTTCAT GAAGGTTCAG TGTCCTAGTT CCCTTCCCCC AGGCAAAACG     960
ACACGGGAGC AGGTCAGGGT TGCTCTGGGT AAAAGCCTGT GAGCCTGGGA GCTAATCCTG    1020
TACATGGCTC CTTTACCTAC ACACTGGGGA TTTGACCTCT ATCTCCACTC TCATTAATAT    1080
GGGTGGCCTA TTTGCTCTTA TTAAAAGGAA AGGGGGAGAT GTTGGGAGCC GCGCCCACAT    1140
TCGCCGTTAC AAGATGGCGC TGACAGCTGT GTTCTAAGTG GTAAACAAAT AATCTGCGCA    1200
TGTGCCGAGG GTGGTTCTTC ACTCCATGTG CTCTGCCTTC CCCGTGACGT CAACTCGGCC    1260
GATGGGCTGC AGCCAATCAG GGAGTGACAC GTCCTAGGCG AAGGAGAATT CTCCTTAATA    1320
GGGACGGGGT TTCGTTCTCT CTCTCTCTCT TGCTTCTCTC TCTTGCTTTT TCGCTCTCTT    1380
GCTTCCCGTA AAGTGATAAT GATTATCATC TACATATCAC AACGTGCGTG GAGG          1434
```

     (2) INFORMATION FOR SEQ ID NO:14:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1400 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: Genomic DNA
     (iii) HYPOTHETICAL: NO
     (iv) ANTISENSE: NO
     (v) FRAGMENT TYPE:
     (vi) ORIGINAL SOURCE:

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA      60
TGTCGACATT TCCACTCCCA ATGACGGTGA TGTATAATGC TCAAGTATTC TCCTGCTTTT     120
TTACCACTAA CTAGGAACTG GGTTTGGCCT TAATTCAGAC AGCCTTGGCT CTGTCTGGAC     180
AGGTCCAGAT ACAACTAGAT GTATTATGAC AAATAACTCA GCAGGGATGT GAACAAAAGT     240
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GGGAATTGAG ACTTCAGGTC AACTCCACGC GCTTGGACCT GTCCCTGACC AAAGGATTAC    420
CCAATTGGAT CTCCTCAGCA TTTTCTTTCT TTAAAAAATG GGTGGGATTA ATATTATTTG    480
GAGATACACT TTGCTGTGGA TTAGTGTTGC TTCTTTGATT GGTCTGTAAG CTTAAGGCCC    540
AAACTAGGAG AGACAAGGTG GTTATTGCCC AGGCGCTTGC AGGACTAGAA CATGGAGCTT    600
CCCCTGATAT ATCTATGCTT AGGCAATAGG TCGCTGGCCA CTCAGCTCTT ATATCCCATG    660
AGGCTAGTCT CATTGCACGG GATAGAGTGA GTGTGCTTCA GCAGCCCGAG AGAGTTGCAC    720
GGCTAAGCAC TGCAATGGAA AGGCTCTGCG GCATATATGA GCCTATTCTA GGGAGACATG    780
TCATCTTTCA AGAAGGTTGA GTGTCCAAGT GTCCTTCCTC CAGGCAAAAC GACACGGGAG    840
CAGGTCAGGG TTGCTCTGGG TAAAAGCCTG TGAGCCTAAG AGCTAATCCT GTACATGGCT    900
CCTTTACCTA CACACTGGGG ATTTGACCTC TATCTCCACT CTCATTAATA TGGGTGGCCT    960
ATTTGCTCTT ATTAAAAGGA AAGGGGGAGA TGTTGGGAGC CGCGCCCACA TTCGCCGTTA   1020
CAAGATGGCG CTGACAGCTG TGTTCTAAGT GGTAAACAAA TAATCTGCGC ATGCGCCGAG   1080
GGTGGTTCTT CACTCCATGT GCTCTGCCTT CCCCGTGACG TCAACTCGGC CGATGGGCTG   1140
CAGTCAATCA GGGAGTGACA CGTCCTAGGC GAAGGAAAAT TCTCCTTAAT AGGGACGGGG   1200
TTTCGTTTTC TCTCTCTCTT GCTTCGCTCT CTCTTGCTTC TTGCTCTCTT TTCCTGAAGA   1260
TGTAAGAATA AAGCTTTGCC GCAGAAGATT CTGGTCTGTG GTGTTCTTCC TGGCCGGTCG   1320
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TATCACAACG TGCGTGGAGG                                                1400
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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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ACACATTACT CAAGGTGGGC TCATCTGAGC TGCAGATTCA GCTTAATATG AATCTTGCCA    180
ATTGTGTGAA ATCATAAATC TTCAAAGTGA CACTCATTGC CAGACACAGG TGCCCACCTT    240
TGGCATAATA AACAAACACA AATTATCTAT TATATAAAGG GTGTTAGAAG ATGCTTTAGA    300
ATACAAATAA ATCATGGTAG ATAACAGTAA GTTGAGAGCT TAAATTTAAT AAAGTGATAT    360
ACCTAATAAA AATTAAATTA AGAAGGTGTG AATATACTAC AGTAGGTAAA TTATTTCATT    420
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ACTATTTCTA CTAGGTGCTA GCTAGTACTG TATTTCGAGA TAGAAGTTAC TGAAAGAAAA   1020
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CACTTATTGG GAATGTTTTT GTTAATAAAA GATTCAGGTG TTACTCTAGG TCAAGAGAAT   1260
ATTAAACATC AGTCCCAAAT TACAAACTTC AATAAAAGAT TTGACTCTCC AGTGGTGGCA   1320
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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22118 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
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CAGACAGACA GACAGACGTT ACAAACAAAC ACGTTGAGCC GTGTGCCAAC ACACACACAA    240
ACACCACTCT GGCCATAATT ATTGAGGACG TTGATTTATT ATTCTGTGTT TGTGAGTCTG    300
TCTGTCTGTC TGTCTGTCTG TCTGTCTGTC TATCAAACCA AAGAAACCA AACAATTATG    360
CCTGCCTGCC TGCCTGCCTG CCTACACAGA GAAATGATTT CTTCAATCAA TCTAAAACGA    420
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CAACCGAGTC ACAGAACAAG GAAGTATACA CAGTGAGTTC CAGGTCAGCC AGAGTTTACA   1140
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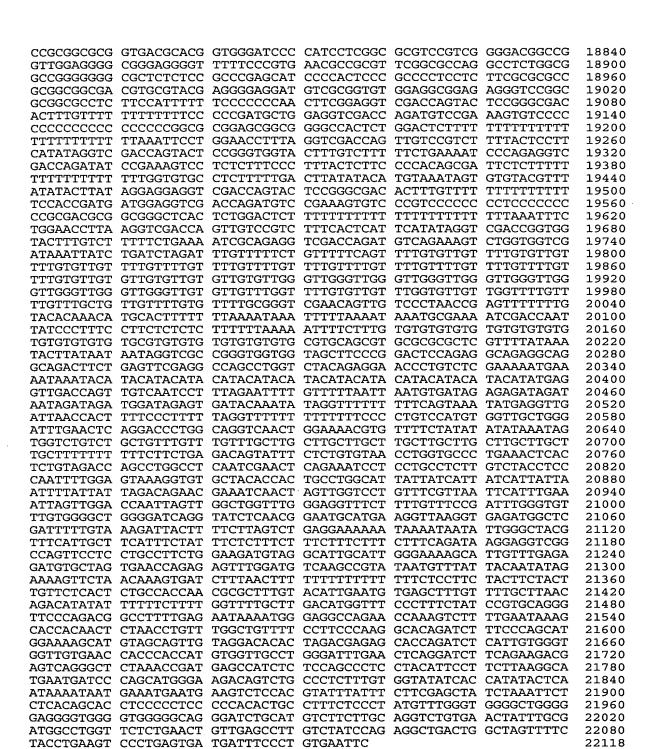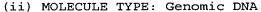
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        (D) TOPOLOGY: linear
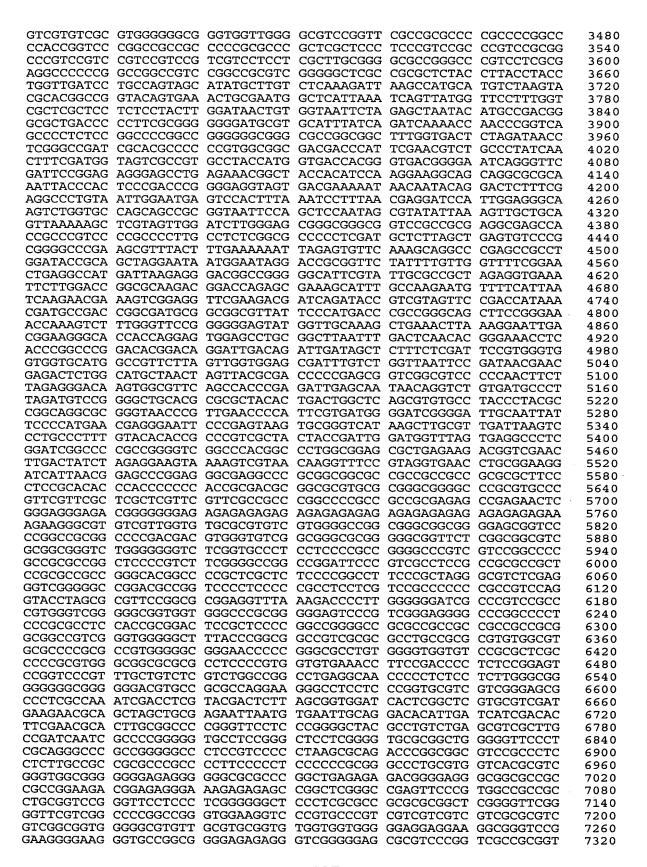
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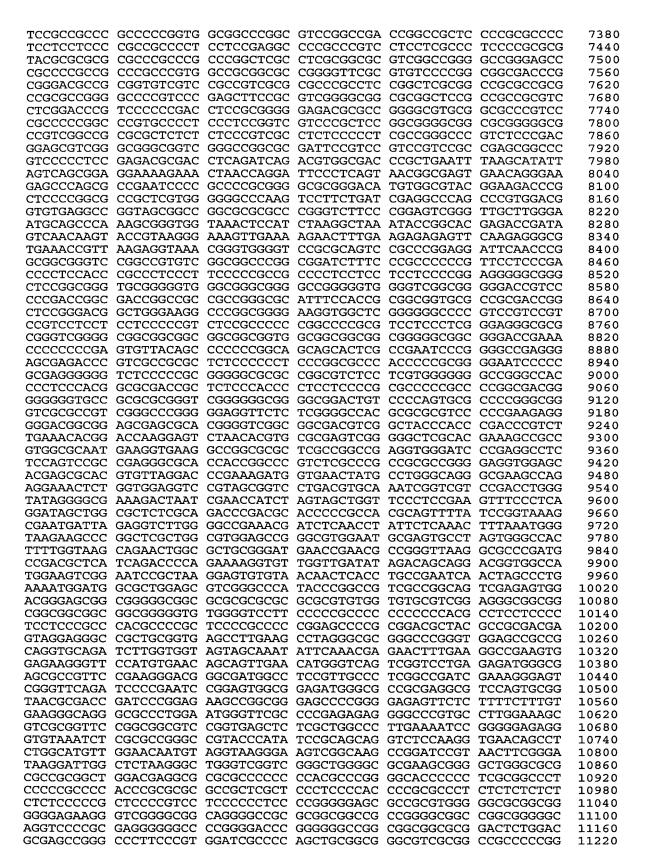(iii) HYPOTHETICAL: NO
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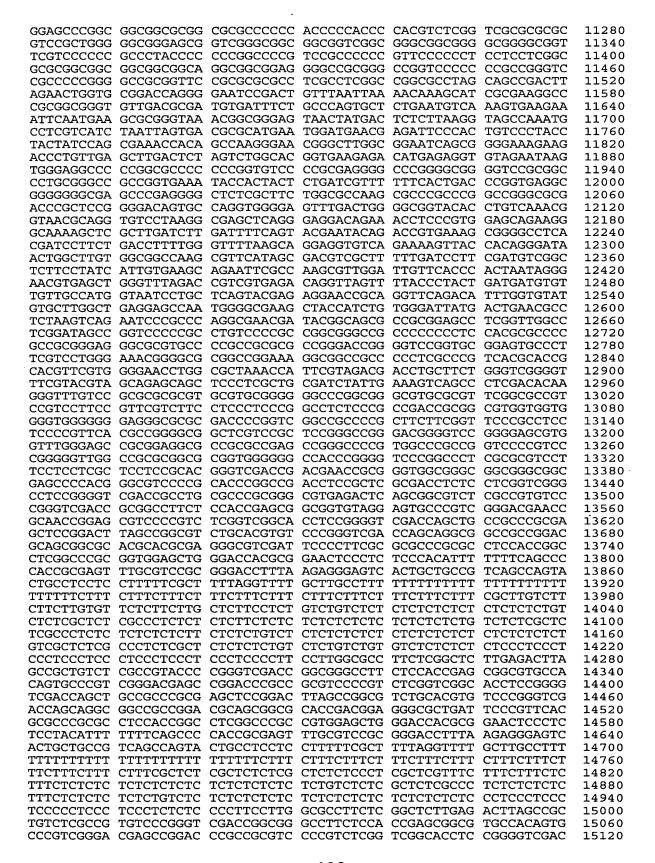(v) FRAGMENT TYPE:
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    (2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 175 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:

    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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    (2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 755 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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    (2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 463 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
GGCCGAGGTG CGTCTGCGGG TTGGGGCTCG TCCGGCCCCG TCGTCCTCCG GGAAGGCGTT    60
TAGCGGGTAC CGTCGCCGCG CCGAGGTGGG CGCACGTCGG TGAGATAACC CCGAGCGTGT   120
TTCTGGTTGT TGGCGGCGGG GGCTCCGGTC GATGTCTTCC CCTCCCCCTC TCCCCGAGGC   180
CAGGTCAGCC TCCGCCTGTG GGCTTCGTCG GCCGTCTCCC CCCCCCTCAC GTCCCTCGCG   240
AGCGAGCCCG TCCGTTCGAC CTTCCTTCCG CCTTCCCCCC ATCTTTCCGC GCTCCGTTGG   300
CCCCGGGGGTT TTCACGGCGC CCCCCACGCT CCTCCGCCTC TCCGCCCGTG GTTTGGACGC   360
CTGGTTCCGG TCTCCCCGCC AAACCCCGGT TGGGTTGGTC TCCGGCCCCG GCTTGCTCTT   420
CGGGTCTCCC AACCCCCGGC CGGAAGGGTT CGGGGGTTCC GGG                      463
```

        (2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 378 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
GGATTCTTCA GGATTGAAAC CCAAACCGGT TCAGTTTCCT TTCCGGCTCC GGCCGGGGGG    60
GGCGGCCCCG GGCGGTTTGG TGAGTTAGAT AACCTCGGGC CGATCGCACG CCCCCCGTGG   120
CGGCGACGAC CCATTCGAAC GTCTGCCCTA TCAACTTTCG ATGGTAGTCG ATGTGCCTAC   180
CATGGTGACC ACGGGTGACG GGGAATCAGG GTTCGATTCC GGAGAGGGAG CCTGAGAAAC   240
GGCTACCACA TCCAAGGAAG GCAGCAGGCG CGCAAATTAC CCACTCCCGA CCCGGGGGAGG   300
TAGTGACGAA AAATAACAAT ACAGGACTCT TTCGAGGCCC TGTAATTGGA ATGAGTCCAC   360
TTTAAATCCT TTAAGCAG                                                  378
```

        (2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 378 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTISENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
GATCCATTGG AGGGCAAGTC TGGTGCCAGC AGCCGCGGTA ATTCCAGCTC CAATAGCGTA    60
TATTAAAGTT GCTGCAGTTA AAAAGCTCGT AGTTGGATCT TGGGAGCGGG CGGGCGGTCC   120
GCCGCGAGGC GAGTCACCGC CCGTCCCCGC CCCTTGCCTC TCGGCGCCCC CTCGATGCTC   180
```

```
TTAGCTGAGT TGTCCCGCGG GGCCCGAAGC GTTTACTTTG AAAAAATTAG AGTTGTTTCA      240
AAGCAGGCCC GAGCCGCCTG GATACCGCCA GCTAGGAAAT AATGGAATAG GACCGCGGTT      300
CCTATTTTGT TTGGTTTTCG GAACTGAGCC CATGATTAAG GGAAACGGCC GGGGGCATTC      360
CCTTATTGCG CCCCCCTA                                                    378
```

          (2) INFORMATION FOR SEQ ID NO:23:

          (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 719 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: Genomic DNA
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
GGATCTTTCC CGCTCCCCGT TCCTCCCGGC CCCTCCACCC GCGCGTCTCC CCCCTTCTTT       60
TCCCCTCTCC GGAGGGGGGG GAGGTGGGGG CGCGTGGGCG GGGTCGGGGG TGGGGTCGGC      120
GGGGGACCGC CCCCGGCCGG CAAAAGGCCG CCGCCGGGCG CACTTCAACC GTAGCGGTGC      180
GCCGCGACCG GCTACGAGAC GGCTGGGAAG GCCCGACGGG GAATGTGGCT CGGGGGGGGC      240
GGCGCGTCTC AGGGCGCGCC GAACCACCTC ACCCCGAGTG TTACAGCCCT CCGGCCGCGC      300
TTTCGCGGAA TCCCGGGGCC GAGGGGAAGC CCGATACCCG TCGCCGCGCT TTTCCCCTCC      360
CCCCGTCCGC CTCCCGGGCG GGCGTGGGGG TGGGGGCCGG GCCGCCCCTC CCACGCCCGT      420
GGTTTCTCTC TCTCCCGGTC TCGGCCGGTT TGGGGGGGGG AGCCCGGTTG GGGGCGGGGC      480
GGACTGTCCT CAGTGCGCCC CGGGCGTCGT CGCGCCGTCG GCCCGGGGG GTTCTCTCGG       540
TCACGCCGCC CCCGACGAAG CCGAGCGCAC GGGGTCGGCG GCGATGTCGG CTACCCACCC      600
GACCCGTCTT GAAACACGGA CCAAGGAGTC TAACGCGTGC GCGAGTCAGG GGCTCGCACG      660
AAAGCCGCCG TGGCGCAATG AAGGTGAAGG GCCCCGTCCG GGGGCCCGAG GTGGGATCC      719
```

          (2) INFORMATION FOR SEQ ID NO:24:

          (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 685 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: Genomic DNA
          (iii) HYPOTHETICAL: NO
          (iv) ANTISENSE: NO
          (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
CGAGGCCTCT CCAGTCCGCC GAGGGCGCAC CACCGGCCCG TCTCGCCCGC CGCGTCGGGG       60
AGGTGGAGCA CGAGCGTACG CGTTAGGACC CGAAAGATGG TGAACTATGC CTGGGCAGGG      120
CGAAGCCAGA GGAAACTCTG GTGGAGGTCC GTAGCGGTCC TGACGTGCAA ATCGGTCGTC      180
CGACCTGGGT ATAGGGGCGA AAGACTAATC GAACCATCTA GTAGCTGGTT CCCTCCGAAG      240
TTTCCCTCAG GATAGCTGGC GCTCTCGCAA CCTTCGGAAG CAGTTTTATC CGGGTAAAGG      300
CGGAATGGAT TAGGAGGTCT TGGGGCCGGA AACGATCTCA AACTATTTCT CAAACTTTAA      360
ATGGGTAAGG AAGCCCGGCT CGCTGGCGTG GAGCCGGGCG TGGAATGCGA GTGCCTAGTG      420
GGCCACTTTT GGTAAGCAGA ACTGGCGCTG CGGGATGAAC CGAACGCCGG GTTAAGGCGC      480
CCGATGCCGA CGCTCATCAG ACCCCAGAAA AGGTGTTGGT TGATATAGAC AGCAGGACGG      540
TGGCCATGGA AGTCGGAATC CGCTAAGGAG TGTGTAACAA CTCACCTGCC GAATCAACTA      600
GCCCTGAAAA TGGATGGCGC TGGAGCGTCG GCCCATACC CGGCCGTCGC CGGCAGTCGG      660
AACGGGACGG GACGGGAGCG GCCGC                                           685
```

          (2) INFORMATION FOR SEQ ID NO:25:

```
(i)  SEQUENCE CHARACTERISTICS:
    (A)  LENGTH: 33 base pairs
    (B)  TYPE: nucleic acid
    (C)  STRANDEDNESS: single
    (D)  TOPOLOGY: linear

(ii)  MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv)  ANTISENSE: NO
(v)   FRAGMENT TYPE:
(vi)  ORIGINAL SOURCE:

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:25:
```

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG   33

```
    (2)  INFORMATION FOR SEQ ID NO:26:

(i)  SEQUENCE CHARACTERISTICS:
    (A)  LENGTH: 35 base pairs
    (B)  TYPE: nucleic acid
    (C)  STRANDEDNESS: single
    (D)  TOPOLOGY: linear

(ii)  MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv)  ANTISENSE: NO
(v)   FRAGMENT TYPE:
(vi)  ORIGINAL SOURCE:

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:26:
```

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG   35

```
    (2)  INFORMATION FOR SEQ ID NO:27:

(i)  SEQUENCE CHARACTERISTICS:
    (A)  LENGTH: 33 base pairs
    (B)  TYPE: nucleic acid
    (C)  STRANDEDNESS: single
    (D)  TOPOLOGY: linear

(ii)  MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv)  ANTISENSE: NO
(v)   FRAGMENT TYPE:
(vi)  ORIGINAL SOURCE:

(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:27:
```

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC   33

```
    (2)  INFORMATION FOR SEQ ID NO:28:

(i)  SEQUENCE CHARACTERISTICS:
    (A)  LENGTH: 34 base pairs
    (B)  TYPE: nucleic acid
    (C)  STRANDEDNESS: single
    (D)  TOPOLOGY: linear

(ii)  MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv)  ANTISENSE: NO
(v)   FRAGMENT TYPE:
(vi)  ORIGINAL SOURCE:
```

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC   34

      (2) INFORMATION FOR SEQ ID NO:29:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 80 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTISENSE: NO
   (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCCT AACCCTAACC CTAACCCTAA   60
CCCTAACCCT AACCCGGGAT   80

      (2) INFORMATION FOR SEQ ID NO:30:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 19 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTISENSE: NO
   (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG   19

      (2) INFORMATION FOR SEQ ID NO:31:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTISENSE: NO
   (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT   25

      (2) INFORMATION FOR SEQ ID NO:32:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single

```
                (D)  TOPOLOGY:  linear

           (ii)  MOLECULE TYPE:  Genomic DNA
           (iii) HYPOTHETICAL:  NO
           (iv)  ANTISENSE:  NO
           (v)   FRAGMENT TYPE:
           (vi)  ORIGINAL SOURCE:

           (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:32:

   GCTGCAAGGC GATTAAGTTG GGTAAC                                    26

            (2)  INFORMATION FOR SEQ ID NO:33:

           (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH:  26 base pairs
              (B)  TYPE:  nucleic acid
              (C)  STRANDEDNESS:  single
              (D)  TOPOLOGY:  linear

           (ii)  MOLECULE TYPE:  Genomic DNA
           (iii) HYPOTHETICAL:  NO
           (iv)  ANTISENSE:  NO
           (v)   FRAGMENT TYPE:
           (vi)  ORIGINAL SOURCE:

           (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:33:

   TATGTTGTGT GGAATTGTGA GCGGAT                                    26

            (2)  INFORMATION FOR SEQ ID NO:34:

           (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH:  21 base pairs
              (B)  TYPE:  nucleic acid
              (C)  STRANDEDNESS:  single
              (D)  TOPOLOGY:  linear

           (ii)  MOLECULE TYPE:  Genomic DNA
           (iii) HYPOTHETICAL:  NO
           (iv)  ANTISENSE:  NO
           (v)   FRAGMENT TYPE:
           (vi)  ORIGINAL SOURCE:

           (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:34:

   GGGTTTAAAC AGATCTCTGC A                                         21
```